

Amendments to the Claims

This listing of claims replaces all prior versions, and listings, of claims in the above-identified application:

1-54. (Canceled)

55. (Currently Amended) A method for crystallizing ~~[[an]]~~ *S. aureus* peptide deformylase ~~molecule or molecular complex~~ comprising:

preparing a stock solution of purified *S. aureus* peptide deformylase at a concentration of about 1 mg/ml to about 50 mg/ml, wherein the amino acid sequence of the *S. aureus* peptide deformylase comprises SEQ ID NO:12;

contacting the stock solution with a precipitating solution containing about 1 % by weight to about 35 % by weight PEG having a number average molecular weight between about 300 and about 20,000; about 0 M to about 0.2 M MgCl_2 ; and about 0 % by weight to about 25 % by weight DMSO; the precipitating solution being buffered to a pH of about 5 to about 9; and allowing *S. aureus* peptide deformylase to crystallize from the resulting solution.

56. (Currently Amended) A method for crystallizing ~~[[an]]~~ *S. aureus* peptide deformylase ~~molecule or molecular complex~~ comprising:

preparing a stock solution of purified *S. aureus* peptide deformylase at a concentration of about 1 mg/ml to about 50 mg/ml, wherein the amino acid sequence of the *S. aureus* peptide deformylase comprises SEQ ID NO:12;

contacting the stock solution with a precipitating solution containing about 1 % by weight to about 40 % by weight PEG having a number average molecular weight between about 300 and about 20,000; about 0.005 M to about 0.5 M citric acid; about 0 % by weight to about 25 % by weight DMSO; and sufficient base to adjust the pH of the precipitating solution to about 5.0 to about 6.5; and

allowing *S. aureus* peptide deformylase to crystallize from the resulting solution.

57. **(Currently Amended)** A method for crystallizing ~~[[an]]~~ *S. aureus* peptide deformylase ~~molecule or molecular complex~~ comprising:

preparing a stock solution of purified *S. aureus* peptide deformylase at a concentration of about 1 mg/ml to about 50 mg/ml, wherein the amino acid sequence of the *S. aureus* peptide deformylase comprises SEQ ID NO:12;

contacting the stock solution with a precipitating solution containing about 0.2 M to about 1.5 M sodium citrate; about 0.005 M to about 0.5 M Hepes; about 0 % by weight to about 25 % by weight DMSO; and sufficient base to adjust the pH of the precipitating solution to about 7.0 to about 8.5; and

allowing *S. aureus* peptide deformylase to crystallize from the resulting solution.

58. **(Currently Amended)** A method for crystallizing ~~[[an]]~~ *S. aureus* peptide deformylase ~~molecule or molecular complex~~ comprising:

preparing a stock solution of purified *S. aureus* peptide deformylase at a concentration of about 1 mg/ml to about 50 mg/ml, wherein the amino acid sequence of the *S. aureus* peptide deformylase comprises SEQ ID NO:12;

contacting the stock solution with a precipitating solution containing about 1 % by weight to about 40 % by weight PEG having a number average molecular weight between about 300 and about 20,000; about 0 M to about 0.4 M MgCl₂; and about 0 % by weight to about 25 % by weight DMSO; the precipitating solution being buffered to a pH of about 7 to about 9; and

allowing *S. aureus* peptide deformylase to crystallize from the resulting solution.

59. **(Currently Amended)** Crystalline *S. aureus* peptide deformylase, wherein the crystalline *S. aureus* peptide deformylase effectively diffracts x-rays to a resolution of 10 Å to 1.9 Å.

60. **(Original)** A crystal of *S. aureus* peptide deformylase having the orthorhombic space

group symmetry $C222_1$.

61. **(Original)** A crystal of *S. aureus* peptide deformylase comprising a unit cell having dimensions a, b, and c; wherein a is about 90 Å to about 100 Å, b is about 116 Å to about 128 Å, and c is about 45 Å to about 50 Å; and wherein $\alpha = \beta = \gamma = 90^\circ$.

62. **(Original)** A crystal of *S. aureus* peptide deformylase having the orthorhombic space group symmetry $C222_1$ and comprising a unit cell having dimensions a, b, and c; wherein a is about 90 Å to about 100 Å, b is about 116 Å to about 128 Å, and c is about 45 Å to about 50 Å; and wherein $\alpha = \beta = \gamma = 90^\circ$.

63. **(Original)** A crystal of *S. aureus* peptide deformylase having the space group symmetry C2 and comprising a unit cell having dimensions a, b, and c; wherein a is about 85 Å to about 100 Å, b is about 35 Å to about 50 Å, and c is about 90 Å to about 110 Å; and wherein $\alpha = \gamma = 90^\circ$ and β is about 90° to about 95° .

64. **(Original)** A crystal of *S. aureus* peptide deformylase having the tetragonal space group symmetry $P4_1$ or $P4_22_12$ and comprising a unit cell having dimensions a, b, and c; wherein a and b are about 130 Å to about 190 Å, and c is about 30 Å to about 70 Å; and wherein $\alpha = \beta = \gamma = 90^\circ$.

65. **(Original)** A crystal of *S. aureus* peptide deformylase comprising atoms arranged in a spatial relationship represented by the structure coordinates listed in Table 1.

66. **(Currently Amended)** A crystal of *S. aureus* peptide deformylase having a single *S. aureus* peptide deformylase molecule as the asymmetric unit, wherein the crystal effectively diffracts x-rays to a resolution of 10 Å to 1.9 Å.

67. **(Currently Amended)** A crystal of *S. aureus* peptide deformylase having an *S. aureus* peptide deformylase amino acid SEQ ID NO:12 ~~SEQ ID NO:1~~, wherein the crystal effectively diffracts x-rays to a resolution of 10 Å to 1.9 Å.
68. **(Currently Amended)** A crystal of *S. aureus* peptide deformylase having a *S. aureus* peptide deformylase amino acid SEQ ID NO:12 ~~SEQ ID NO:1~~, except that at least one methionine is replaced with selenomethionine, wherein the crystal effectively diffracts x-rays to a resolution of 10 Å to 1.9 Å.
69. **(Currently Amended)** A crystal of *S. aureus* peptide deformylase having a coordinated metal ion selected from the group of metals consisting of Fe, Zn, Ni and combinations thereof, wherein the crystal effectively diffracts x-rays to a resolution of 10 Å to 1.9 Å.
70. **(New)** A polypeptide consisting of a portion of *S. aureus* peptide deformylase starting at amino acid 58 and ending at amino acid 158 of *S. aureus* peptide deformylase as set forth in SEQ ID NO:12.
71. **(New)** The polypeptide of claim 70, wherein the three-dimensional configuration of amino acids Gly58, Gly60, Leu61, Gln65, Glu109, Gly110, Cys111, Leu112, Ile150, His154, Glu155, and His158, is defined by a set of points having a root mean square deviation of less than about 0.35 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.
72. **(New)** The polypeptide of claim 71, wherein the three-dimensional configuration of all the amino acids is defined by a set of points having a root mean square deviation of less than about 0.35 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

73. (New) The polypeptide of claim 70 further comprising a coordinated metal ion selected from the group of metals consisting of Fe, Zn, Ni and combinations thereof.

74. (New) The polypeptide of claim 73, wherein the metal ion is coordinated by amino acids Cys111, His154, and His158.

75. (New) A polypeptide consisting of a portion of *S. aureus* peptide deformylase starting at amino acid 56 and ending at amino acid 158 of *S. aureus* peptide deformylase as set forth in SEQ ID NO:12.

76. (New) The polypeptide of claim 75, wherein the three-dimensional configuration of amino acids Arg56, Ser57, Gly58, Val59, Gly60, Leu61, Gln65, Leu105, Pro106, Thr107, Gly108, Glu109, Gly110, Cys111, Leu112, Asn117, Tyr147, Ile150, Val151, His154, Glu155, and His158, is defined by a set of points having a root mean square deviation of less than about 0.8 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

77. (New) The polypeptide of claim 76, wherein the three-dimensional configuration of all the amino acids is defined by a set of points having a root mean square deviation of less than about 0.8 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

78. (New) The polypeptide of claim 75 further comprising a coordinated metal ion selected from the group of metals consisting of Fe, Zn, Ni and combinations thereof.

79. (New) The polypeptide of claim 78, wherein the metal ion is coordinated by amino acids Cys111, His154, and His158.